



SEQUENCE LISTING

#7

<110> Duke University
Lin, Haifan

<120> PURIFIED AND ISOLATED piwi FAMILY GENES AND GENE
PRODUCTS AND THERAPEUTIC AND SCREENING METHODS USING SAME

<130> Attorney Docket No. 180-104/2

<140> 09/873,737

<141> 2001-06-04

<150> PCT/US99/28764

<151> 1999-12-03

<150> 60/110,901

<151> 1998-12-04

<160> 21

<170> PatentIn Ver. 2.1

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Arg Pro Xaa Asn Glu Asp Asp Ser Ser Thr Ser Arg Gly Ser Gly Asp
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Pro Gly Tyr Glu Thr Ser Ile Arg Gln His Glu Lys Asp Ile Leu Leu	
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Leu			
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 Arg Ser Leu Met Ser Ile Ala Thr Lys Ile Ala Ile Gln Leu Asn Cys
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 Glu Lys Leu Lys Thr Glu Tyr Ala Arg Val Gln Leu Ser Pro Pro Gln
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 Pro Gly Tyr Ile Pro Pro Arg Pro Gln Gln Ser Pro Thr Glu Gly Asp
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 Leu Val Gly Arg Gly Arg Gln Arg Gly Met Val Val Gly Ala Thr Ser
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 Lys Ser Gln Glu Leu Gln Ile Ser Ala Gly Phe Gln Glu Leu Ser Leu
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 Ala Glu Arg Gly Gly Arg Arg Asp Phe His Asp Xaa Gly Val Asn
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 Gly Ile Ile Val Lys Leu Ser Thr Asn His Phe Arg Leu Thr Ser Arg
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Thr	Pro	Glu	Gln	Arg	Gln	Arg	Glu	Val	Gly	Arg	Leu	Ile	Asp	Tyr	Ile		
	415					420					425						
cac	aag	gat	gac	aat	gtg	cag	aga	gag	ctt	cga	gac	tgg	ggc	ctg	agc	1525	
His	Lys	Asp	Asp	Asn	Val	Gln	Arg	Glu	Leu	Arg	Asp	Trp	Gly	Leu	Ser		
430					435					440					445		
ttc	gac	tca	aac	ttg	ctg	tcc	ttc	tct	gga	aga	atc	tta	caa	tct	gag	1573	
Phe	Asp	Ser	Asn	Leu	Leu	Ser	Phe	Ser	Gly	Arg	Ile	Leu	Gln	Ser	Glu		

450										455										460										
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Lys Ile His Gln Gly Gly Lys Thr Phe Asp Tyr Asn Pro Gln Phe Ala																														
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480 485 490																														
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Leu Asp Asn Trp Leu Leu Ile Tyr Thr Arg Arg Asn Tyr Glu Ala Ala																														
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Gln Met Lys Lys Ala Ile Met Ile Glu Val Asp Asp Arg Thr Glu Ala																														
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Tyr Leu Arg Ala Leu Gln Gln Lys Val Thr Ser Asp Thr Gln Ile Val																														
545 550 555																														
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Val Cys Leu Leu Ser Ser Asn Arg Lys Asp Lys Tyr Asp Ala Ile Lys																														
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aag tac ttg tgt aca gac tgc ccc acc cca agt cag tgt gtg gtg gcc	1957																													
Lys Tyr Leu Cys Thr Asp Cys Pro Thr Pro Ser Gln Cys Val Val Ala																														
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cgg acc ctg ggc aag cag caa aca gtc atg gcc att gcc acc aag atc	2005																													
Arg Thr Leu Gly Lys Gln Gln Thr Val Met Ala Ile Ala Thr Lys Ile																														
590 595 600 605																														
gcc ctg cag atg aac tgc aag atg gga ggc gag ctc tgg cgg gtg gac	2053																													
Ala Leu Gln Met Asn Cys Lys Met Gly Gly Glu Leu Trp Arg Val Asp																														
610 615 620																														
atg gcc ctg aaa ctg gca atg atc gtg ggc atc gac tgt tac cat gac	2101																													
Met Ala Leu Lys Leu Ala Met Ile Val Gly Ile Asp Cys Tyr His Asp																														
625 630 635																														
acc aca gct ggg cgg agg tcc atc gca gga ttc gtc gcc agc atc aat	2149																													
Thr Thr Ala Gly Arg Arg Ser Ile Ala Gly Phe Val Ala Ser Ile Asn																														
640 645 650																														
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Glu Gly Met Thr Arg Trp Phe Ser Arg Cys Val Phe Gln Asp Arg Gly																														
655 660 665																														
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Gln Glu Leu Val Asp Gly Leu Lys Val Cys Leu Gln Ala Ala Leu Arg																														
670 675 680 685																														
gct tgg agt ggc tgc aat gaa tac atg ccc agc cgt gtc atc gtg tac	2293																													
Ala Trp Ser Gly Cys Asn Glu Tyr Met Pro Ser Arg Val Ile Val Tyr																														
690 695 700																														

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 Arg Asp Gly Val Gly Asp Gly Gln Leu Lys Thr Leu Val Asn Tyr Glu
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 Val Pro Gln Phe Leu Asp Cys Leu Lys Ser Val Gly Arg Gly Tyr Asn
 720 725 730

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 Pro Arg Leu Thr Val Ile Val Val Lys Lys Arg Val Asn Ala Arg Phe
 735 740 745

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 Phe Ala Gln Ser Gly Gly Arg Leu Gln Asn Pro Leu Pro Gly Thr Val
 750 755 760 765

atc gat gtg gaa gtc acc aga cca gag tgg tat gac ttt ttc atc gtg 2533
 Ile Asp Val Glu Val Thr Arg Pro Glu Trp Tyr Asp Phe Phe Ile Val
 770 775 780

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 Ser Gln Ala Val Arg Ser Gly Ser Val Ser Pro Thr His Tyr Asn Val
 785 790 795

atc tat gac agc agt ggc ctg aag ccc gac cac atc cag cgg ctg aca 2629
 Ile Tyr Asp Ser Ser Gly Leu Lys Pro Asp His Ile Gln Arg Leu Thr
 800 805 810

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 Tyr Lys Xaa Cys His Val Tyr Tyr Asn Trp Pro Gly Val Ile Arg Val
 815 820 825

cct gca cct tgc cag tat gca cac aag ctg gcc ttc ctc gtg ggc cag 2725
 Pro Ala Pro Cys Gln Tyr Ala His Lys Leu Ala Phe Leu Val Gly Gln
 830 835 840 845

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 Ser Ile His Arg Glu Pro Asn Leu Ser Leu Ser Asn Arg Leu Tyr Tyr
 850 855 860

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 Leu

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 35 40 45

Arg Gly Arg Gln Arg Gly Met Val Val Gly Ala Thr Ser Lys Ser Gln
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 Glu Leu Gln Ile Ser Ala Gly Phe Gln Glu Leu Ser Leu Ala Glu Arg
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 Gly Gly Arg Arg Arg Asp Phe His Asp Xaa Gly Val Asn Thr Arg Gln
 85 90 95
 Asn Leu Asp His Val Lys Glu Ser Lys Thr Gly Ser Ser Gly Ile Ile
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 Val Lys Leu Ser Thr Asn His Phe Arg Leu Thr Ser Arg Pro Gln Trp
 115 120 125
 Ala Leu Tyr Gln Tyr His Ile Asp Tyr Asn Pro Leu Met Glu Ala Arg
 130 135 140
 Arg Leu Arg Ser Ala Leu Leu Phe Gln His Glu Asp Leu Ile Gly Arg
 145 150 155 160
 Cys His Ala Phe Asp Gly Thr Ile Leu Phe Leu Pro Lys Arg Leu Gln
 165 170 175
 His Lys Val Thr Glu Val Phe Ser Gln Thr Arg Asn Gly Glu His Val
 180 185 190
 Arg Ile Thr Ile Thr Leu Thr Asn Glu Leu Pro Pro Thr Ser Pro Thr
 195 200 205
 Cys Leu Gln Phe Tyr Asn Ile Xaa Phe Arg Arg Leu Leu Lys Ile Met
 210 215 220
 Asn Leu Gln Gln Ile Gly Arg Asn Tyr Tyr Asn Pro Ser Asp Pro Ile
 225 230 235 240
 Asp Ile Pro Asn His Arg Leu Val Ile Trp Pro Gly Phe Thr Thr Ser
 245 250 255
 Ile Leu Gln Tyr Glu Asn Asn Ile Met Leu Cys Thr Asp Val Ser His
 260 265 270
 Lys Val Leu Arg Ser Glu Thr Val Leu Asp Phe Met Phe Asn Leu Tyr
 275 280 285
 Gln Gln Thr Glu Glu His Lys Phe Gln Glu Gln Val Ser Lys Glu Leu
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 Ile Gly Leu Ile Val Leu Thr Lys Tyr Asn Asn Lys Thr Tyr Arg Val
 305 310 315 320
 Asp Asp Ile Asp Trp Asp Gln Asn Pro Lys Ser Thr Phe Lys Lys Ala
 325 330 335
 Asp Gly Ser Glu Val Ser Phe Leu Glu Tyr Tyr Arg Lys Gln Tyr Asn
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 Gln Glu Ile Thr Asp Leu Lys Gln Pro Val Leu Val Ser Gln Pro Lys
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 Arg Arg Arg Gly Pro Gly Gly Thr Leu Pro Gly Pro Ala Met Xaa Ile

370	375	380
Pro Glu Leu Cys Tyr	Leu Thr Gly Leu Thr	Asp Lys Met Arg Asn Asp
385	390	395 400
Phe Asn Val Met Lys	Asp Leu Ala Val His Thr Arg Leu Thr	Pro Glu
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Gln Arg Gln Arg Glu Val Gly Arg	Leu Ile Asp Tyr Ile His Lys Asp	
420	425	430
Asp Asn Val Gln Arg Glu Leu Arg	Asp Trp Gly Leu Ser Phe Asp Ser	
435	440	445
Asn Leu Leu Ser Phe Ser Gly Arg Ile Leu Gln Ser Glu Lys Ile His		
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Gln Gly Gly Lys Thr Phe Asp Tyr Asn Pro Gln Phe Ala Asp Trp Ser		
465	470	475 480
Lys Glu Thr Arg Gly Ala Pro Leu Ile Ser Val Lys Pro Leu Asp Asn		
485	490	495
Trp Leu Leu Ile Tyr Thr Arg Arg Asn Tyr Glu Ala Ala Asn Ser Leu		
500	505	510
Ile Gln Asn Leu Phe Lys Val Thr Pro Ala Met Gly Ile Gln Met Lys		
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Lys Ala Ile Met Ile Glu Val Asp Asp Arg Thr Glu Ala Tyr Leu Arg		
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Ala Leu Gln Gln Lys Val Thr Ser Asp Thr Gln Ile Val Val Cys Leu		
545	550	555 560
Leu Ser Ser Asn Arg Lys Asp Lys Tyr Asp Ala Ile Lys Lys Tyr Leu		
565	570	575
Cys Thr Asp Cys Pro Thr Pro Ser Gln Cys Val Val Ala Arg Thr Leu		
580	585	590
Gly Lys Gln Gln Thr Val Met Ala Ile Ala Thr Lys Ile Ala Leu Gln		
595	600	605
Met Asn Cys Lys Met Gly Gly Glu Leu Trp Arg Val Asp Met Ala Leu		
610	615	620
Lys Leu Ala Met Ile Val Gly Ile Asp Cys Tyr His Asp Thr Thr Ala		
625	630	635 640
Gly Arg Arg Ser Ile Ala Gly Phe Val Ala Ser Ile Asn Glu Gly Met		
645	650	655
Thr Arg Trp Phe Ser Arg Cys Val Phe Gln Asp Arg Gly Gln Glu Leu		
660	665	670
Val Asp Gly Leu Lys Val Cys Leu Gln Ala Ala Leu Arg Ala Trp Ser		
675	680	685
Gly Cys Asn Glu Tyr Met Pro Ser Arg Val Ile Val Tyr Arg Asp Gly		
690	695	700

Val Gly Asp Gly Gln Leu Lys Thr Leu Val Asn Tyr Glu Val Pro Gln
 705 710 715 720
 Phe Leu Asp Cys Leu Lys Ser Val Gly Arg Gly Tyr Asn Pro Arg Leu
 725 730 735
 Thr Val Ile Val Val Lys Lys Arg Val Asn Ala Arg Phe Phe Ala Gln
 740 745 750
 Ser Gly Gly Arg Leu Gln Asn Pro Leu Pro Gly Thr Val Ile Asp Val
 755 760 765
 Glu Val Thr Arg Pro Glu Trp Tyr Asp Phe Phe Ile Val Ser Gln Ala
 770 775 780
 Val Arg Ser Gly Ser Val Ser Pro Thr His Tyr Asn Val Ile Tyr Asp
 785 790 795 800
 Ser Ser Gly Leu Lys Pro Asp His Ile Gln Arg Leu Thr Tyr Lys Xaa
 805 810 815
 Cys His Val Tyr Tyr Asn Trp Pro Gly Val Ile Arg Val Pro Ala Pro
 820 825 830
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 aggaccagga ctagggcgag ggcagcggtc caagaaatag aaaaca atg act ggg 175

Met Thr Gly

1

aga gcc cga gcc aga gcc aga gga agg gcc cgc ggt cag gag aca gcg	223
Arg Ala Arg Ala Arg Ala Arg Gly Arg Ala Arg Gly Gln Glu Thr Ala	
5 10 15	
cag ctg gtg ggc tcc act gcc agt cag caa cct ggt tat att cag cct	271
Gln Leu Val Gly Ser Thr Ala Ser Gln Gln Pro Gly Tyr Ile Gln Pro	
20 25 30 35	
agg cct cag ccg cca cca gca gag ggg gaa tta ttt ggc cgt gga cgg	319
Arg Pro Gln Pro Pro Pro Ala Glu Gly Glu Leu Phe Gly Arg Gly Arg	
40 45 50	
cag aga gga aca gca gga gga aca gcc aag tca caa gga ctc cag ata	367
Gln Arg Gly Thr Ala Gly Gly Thr Ala Lys Ser Gln Gly Leu Gln Ile	
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tct gct gga ttt cag gag tta tcg nta gca gag aga gga ggt cgt cgt	415
Ser Ala Gly Phe Gln Glu Leu Ser Xaa Ala Glu Arg Gly Gly Arg Arg	
70 75 80	
aga gat ttt cat gat ctt ggt gtg aat aca agg cag aac cta gac cat	463
Arg Asp Phe His Asp Leu Gly Val Asn Thr Arg Gln Asn Leu Asp His	
85 90 95	
gtt aaa gaa tca aaa aca ggt tct tca ggc att ata gta agg tta agc	511
Val Lys Glu Ser Lys Thr Gly Ser Ser Gly Ile Ile Val Arg Leu Ser	
100 105 110 115	
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Thr Asn His Phe Arg Leu Thr Ser Arg Pro Gln Trp Ala Leu Tyr Gln	
120 125 130	
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Tyr His Ile Asp Tyr Asn Pro Leu Met Glu Ala Arg Arg Leu Arg Ser	
135 140 145	
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Ala Leu Leu Phe Gln His Glu Asp Leu Ile Gly Lys Cys His Ala Phe	
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Asp Gly Thr Ile Leu Phe Leu Pro Lys Arg Leu Gln Gln Lys Val Thr	
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Thr Leu Thr Asn Glu Leu Pro Pro Thr Ser Pro Thr Cys Leu Gln Phe	
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Ile Gly Arg Asn Tyr Tyr Asn Pro Asn Asp Pro Ile Asp Ile Pro Ser	

230	235	240	
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gaa cat aaa ttt caa gaa caa gtt tcc aaa gaa nta ata ggt tta gtt Glu His Lys Phe Gln Glu Gln Val Ser Lys Glu Xaa Ile Gly Leu Val 295 300 305			1087
gtt ctt acc aag tat aac att aag aca tac aga gtg gat gat att gac Val Leu Thr Lys Tyr Asn Ile Lys Thr Tyr Arg Val Asp Asp Ile Asp 310 315 320			1135
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Val Lys Lys Arg Val Asn Thr Arg Phe Phe Ala Gln Ser Gly Gly Arg	
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760 765 770	
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Pro Glu Trp Tyr Asp Phe Phe Ile Val Ser Gln Ala Val Arg Ser Gly	
775 780 785	
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Ser Val Ser Pro Thr His Tyr Asn Val Ile Tyr Asp Asn Ser Gly Leu	
790 795 800	
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Lys Pro Asp His Ile Gln Arg Leu Thr Tyr Lys Leu Cys His Ile Tyr	
805 810 815	
tac aac tgg cca ggt gtc att cgt gtt cct gct cct tgc cag tac gcc	2671
Tyr Asn Trp Pro Gly Val Ile Arg Val Pro Ala Pro Cys Gln Tyr Ala	
820 825 830 835	
cac aag ctg gct ttt ctt gtt ggc cag agt att cac aga gag cca aat	2719
His Lys Leu Ala Phe Leu Val Gly Gln Ser Ile His Arg Glu Pro Asn	
840 845 850	
ctg tca ctg tca aac cgc ctt tac tac ctc taacctgcag aagacgatgc	2769
Leu Ser Leu Ser Asn Arg Leu Tyr Tyr Leu	
855 860	
agccgctttt ctttttgaaa tgactttggg atttttttaa gcttttattt actttttttt	2829
taactgttat ctttctggat gaaacttggg aaggggatta ggagatctag cattttattt	2889
ctagcattgc tattcacggg cttccttatt ttatatgtaa aaattaagat tttatatattt	2949
atcttcttgt ttctcataga tattttgtga gcattttttt gtttattttg aagaaatgtg	3009
gataagatac ttggtagtat aaaacagact ctctgagagt atttgaaatg tgtttggaga	3069
tttacttaaa cgtactttca ggagtgcagc agtcctactt ataaacctat attaaactta	3129
tttttgagat acctgttttg aatttaaagg agataagagg cgtaaagtag gatgctcact	3189
acaaccatag gtgggggttc agctcatatc ttaaagataa aagggtactat tatataacct	3249
atacacaaga tacaggagaa aatatgcttg atttttattt ggcagggggg ctaggttgta	3309
tgggagtaaa aaaaacattg aaaattttta aattgtccaa agaaacattt taagactctt	3369
taacaaaaaa ggccatgagt aaatctctat attaacatca ctatttattt tgttttgga	3429
ctgggacatg attctatttg ttataaaata aaattgatgt ccc	3472

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Glu Thr Ala Gln Leu Val Gly Ser Thr Ala Ser Gln Gln Pro Gly Tyr
20 25 30
Ile Gln Pro Arg Pro Gln Pro Pro Pro Ala Glu Gly Glu Leu Phe Gly
35 40 45
Arg Gly Arg Gln Arg Gly Thr Ala Gly Gly Thr Ala Lys Ser Gln Gly
50 55 60
Leu Gln Ile Ser Ala Gly Phe Gln Glu Leu Ser Xaa Ala Glu Arg Gly
65 70 75 80
Gly Arg Arg Arg Asp Phe His Asp Leu Gly Val Asn Thr Arg Gln Asn
85 90 95
Leu Asp His Val Lys Glu Ser Lys Thr Gly Ser Ser Gly Ile Ile Val
100 105 110
Arg Leu Ser Thr Asn His Phe Arg Leu Thr Ser Arg Pro Gln Trp Ala
115 120 125
Leu Tyr Gln Tyr His Ile Asp Tyr Asn Pro Leu Met Glu Ala Arg Arg
130 135 140
Leu Arg Ser Ala Leu Leu Phe Gln His Glu Asp Leu Ile Gly Lys Cys
145 150 155 160
His Ala Phe Asp Gly Thr Ile Leu Phe Leu Pro Lys Arg Leu Gln Gln
165 170 175
Lys Val Thr Glu Val Phe Ser Lys Thr Arg Asn Gly Glu Asp Val Arg
180 185 190
Ile Thr Ile Thr Leu Thr Asn Glu Leu Pro Pro Thr Ser Pro Thr Cys
195 200 205
Leu Gln Phe Tyr Asn Ile Ile Phe Arg Arg Leu Leu Lys Ile Met Asn

210	215	220
Leu Gln Gln Ile Gly Arg Asn Tyr Tyr Asn Pro Asn Asp Pro Ile Asp 225 230 235 240		
Ile Pro Ser His Arg Leu Val Ile Trp Pro Gly Phe Thr Thr Ser Ile 245 250 255		
Leu Gln Tyr Glu Asn Ser Ile Met Leu Cys Thr Asp Val Ser His Lys 260 265 270		
Val Leu Arg Ser Glu Thr Val Leu Asp Phe Met Phe Asn Phe Tyr His 275 280 285		
Gln Thr Glu Glu His Lys Phe Gln Glu Gln Val Ser Lys Glu Xaa Ile 290 295 300		
Gly Leu Val Val Leu Thr Lys Tyr Asn Ile Lys Thr Tyr Arg Val Asp 305 310 315 320		
Asp Ile Asp Trp Asp Gln Asn Pro Lys Ser Thr Phe Lys Lys Ala Asp 325 330 335		
Gly Ser Gly Val Ser Phe Leu Glu Tyr Tyr Arg Lys Gln Tyr Asn Gln 340 345 350		
Glu Ile Thr Asp Leu Lys Gln Pro Val Leu Val Ser Gln Pro Lys Arg 355 360 365		
Arg Arg Gly Pro Gly Gly Thr Leu Pro Gly Pro Ala Met Leu Ile Pro 370 375 380		
Glu Leu Cys Tyr Leu Thr Gly Leu Thr Asp Lys Met Arg Asn Asp Phe 385 390 395 400		
Asn Val Met Lys Asp Leu Ala Val His Thr Arg Leu Thr Pro Glu Gln 405 410 415		
Arg Gln Arg Glu Val Gly Arg Leu Ile Asp Tyr Ile His Lys Asn Asp 420 425 430		
Asn Val Gln Arg Glu Leu Arg Asp Trp Gly Leu Ser Phe Asp Ser Asn 435 440 445		
Leu Leu Ser Phe Ser Gly Arg Ile Leu Gln Thr Glu Lys Ile His Gln 450 455 460		
Gly Gly Lys Thr Phe Asp Tyr Asn Pro Gln Phe Ala Asp Trp Ser Lys 465 470 475 480		
Glu Thr Arg Gly Ala Pro Leu Ile Ser Val Lys Pro Leu Asp Asn Trp 485 490 495		
Leu Leu Ile Tyr Thr Arg Arg Asn Tyr Glu Ala Ala Asn Ser Leu Ile 500 505 510		
Gln Asn Leu Phe Lys Val Thr Pro Ala Met Gly Met Gln Met Arg Lys 515 520 525		
Ala Ile Met Ile Glu Val Asp Asp Arg Thr Glu Ala Tyr Leu Arg Val 530 535 540		

Leu Gln Gln Lys Val Thr Ala Asp Thr Gln Ile Val Val Cys Leu Leu
 545 550 555 560
 Ser Ser Asn Arg Lys Asp Lys Tyr Asp Ala Ile Lys Lys Tyr Leu Cys
 565 570 575
 Thr Asp Cys Pro Thr Pro Ser Gln Cys Val Val Ala Arg Thr Leu Gly
 580 585 590
 Lys Gln Gln Thr Val Met Ala Ile Ala Thr Lys Ile Ala Leu Gln Met
 595 600 605
 Asn Cys Lys Met Gly Gly Glu Leu Trp Arg Val Asp Ile Pro Leu Lys
 610 615 620
 Leu Val Met Ile Val Gly Ile Asp Cys Tyr His Asp Met Thr Ala Gly
 625 630 635 640
 Arg Arg Ser Ile Ala Gly Phe Val Ala Ser Ile Asn Glu Gly Met Thr
 645 650 655
 Arg Trp Phe Ser Arg Cys Ile Phe Gln Asp Arg Gly Gln Glu Leu Val
 660 665 670
 Asp Gly Leu Lys Val Cys Leu Gln Ala Ala Leu Arg Ala Trp Asn Ser
 675 680 685
 Cys Asn Glu Tyr Met Pro Ser Arg Ile Ile Val Tyr Arg Asp Gly Val
 690 695 700
 Gly Asp Gly Gln Leu Lys Thr Leu Val Asn Tyr Glu Val Pro Gln Phe
 705 710 715 720
 Leu Asp Cys Leu Lys Ser Ile Gly Arg Gly Tyr Asn Pro Arg Xaa Thr
 725 730 735
 Val Ile Val Val Lys Lys Arg Val Asn Thr Arg Phe Phe Ala Gln Ser
 740 745 750
 Gly Gly Arg Leu Gln Asn Pro Leu Pro Gly Thr Val Ile Asp Val Glu
 755 760 765
 Val Thr Arg Pro Glu Trp Tyr Asp Phe Phe Ile Val Ser Gln Ala Val
 770 775 780
 Arg Ser Gly Ser Val Ser Pro Thr His Tyr Asn Val Ile Tyr Asp Asn
 785 790 795 800
 Ser Gly Leu Lys Pro Asp His Ile Gln Arg Leu Thr Tyr Lys Leu Cys
 805 810 815
 His Ile Tyr Tyr Asn Trp Pro Gly Val Ile Arg Val Pro Ala Pro Cys
 820 825 830
 Gln Tyr Ala His Lys Leu Ala Phe Leu Val Gly Gln Ser Ile His Arg
 835 840 845
 Glu Pro Asn Leu Ser Leu Ser Asn Arg Leu Tyr Tyr Leu
 850 855 860

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Oligonucleotide Primer

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<220>
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Oligonucleotide Primer

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<210> 10
<211> 45
<212> DNA
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Oligonucleotide Primer

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<210> 11
<211> 17
<212> DNA
<213> Artificial Sequence
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Oligonucleotide Primer

<400> 11
acgataagtt ctgttat 17

<210> 12
 <211> 23
 <212> DNA
 <213> Artificial Sequence
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 Oligonucleotide Primer

 <400> 12
 tgcactgccca ggctccttcat cac 23

 <210> 13
 <211> 29
 <212> DNA
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 Oligonucleotide Primer

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 <212> DNA
 <213> Artificial Sequence
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 <223> Description of Artificial Sequence: Synthesized
 Oligonucleotide Primer

 <400> 14
 atgggggtcctt ttcttgcctca 20

 <210> 15
 <211> 20
 <212> DNA
 <213> Artificial Sequence
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 <223> Description of Artificial Sequence: Synthesized
 Oligonucleotide Primer

 <400> 15
 tgcccattaa catcaccatc 20

 <210> 16
 <211> 24
 <212> DNA
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 Oligonucleotide Primer

 <400> 16
 tgatttggggg acttatttta gagc 24

 <210> 17

<211> 23
<212> DNA
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<223> Description of Artificial Sequence: Synthesized
Oligonucleotide Primer

<400> 17
acttaccttg tgacttgat gtg

23

<210> 18
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<212> DNA
<213> Artificial Sequence
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Oligonucleotide Primer

<400> 18
ttgaaaagca ttgaacacca taag

24

<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthesized
Oligonucleotide Primer

<400> 19
gataaccacc gcctgcctt tcac

24

<210> 20
<211> 20
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthesized
Oligonucleotide Primer

<400> 20
tgcccattaa catcaccatc

20

<210> 21
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<400> 21
Pro Pro Arg Gln